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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=22; hr=8; min=18; sec=15; ms=873;]

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Application No: 10587956 Version No: 2.0

Input Set:

Output Set:

Started: 2010-01-06 16:58:26.791
Finished: 2010-01-06 16:58:28.474
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 683 ms
Total Warnings: 15
Total Errors: 0
No. of SeqIDs Defined: 19
Actual SeqID Count: 19

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SEQUENCE LISTING

<110> Korea Research Institute of Bioscience and Biotechnology
Kang, Hyun-As
Kim, Moo-Woong
Rhee, Sang-Ki
Heo, Joo Hyung

<120> Novel Hansenula Polymorpha Gene Coding for Alpha
1,6-Mannosyltransferase and Process for the Production of
Recombinant Glycoproteins with Hansenula Polymorpha Mutant Strain
Deficient in the Same Gene

<130> HANOL-13037

<140> 10587956
<141> 2010-01-06

<150> PCT/KR 2004/001819
<151> 2004-07-21

<150> KR 10-2004-0006352
<151> 2004-01-30

<160> 19

<170> PatentIn version 3.5

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<212> DNA
<213> Hansenula polymorpha

<220>
<221> CDS
<222> (10)..(1293)

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gtg ctg aag cgc gcg cga ctc tac atg gcg acg aat cgc cgg ctg gtg 99
Val Leu Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val
15 20 25 30

gtt gtt ctt gtg gtg ctg ctg tac tgg gtg gtc cag aac gtt tgg acg 147
Val Val Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr
35 40 45

tgg agc cct ggg acg cgc gat ttg gcc caa gtg gac gcg aag atc gag 195
Trp Ser Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu
50 55 60

gcc gag cta aac tcg aat cta cat act ttt gga gcg cat ttg cgc cac 243

Ala Glu Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His	
65 70 75	
tta aac cgg ctt ccg gca gag tcg gcc acc ctg cgt gaa aaa ctc acc	291
Leu Asn Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr	
80 85 90	
ttc tat ttc cca tat tat cct gaa aag ccc gtg ccg aac cag atc tgg	339
Phe Tyr Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp	
95 100 105 110	
cag aca tgg aag gtc gat ctc gaa gac gac aac ttc ccc aag cag tac	387
Gln Thr Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr	
115 120 125	
aga cgg ttt cag aag acg tgg gtc gag aaa aat cca gac tac gtg tac	435
Arg Arg Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr	
130 135 140	
cac ctg att ccg gac tct gtg att gag gac ttt gtg gcg agt ttg tac	483
His Leu Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr	
145 150 155	
gcg aac gtg ccg gag gtg gtc aga gcg tac cag ctg ctt ccg aaa aat	531
Ala Asn Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn	
160 165 170	
atc atg aag gcg gat ttt ttc cgg tat ttg gtg atc tac gcg cgc gga	579
Ile Met Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly	
175 180 185 190	
ggc acc tac tca gac atg gac acg gtg tgt tta aag ccg atc aag gac	627
Gly Thr Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp	
195 200 205	
tgg gcc acg ttt gat cgc gac ctg atc cac gct gcc gac aat aag gcc	675
Trp Ala Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala	
210 215 220	
gat ctc tcc cag ata gat cca gaa gca aga acc acg cct gtg ggg ctg	723
Asp Leu Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu	
225 230 235	
gtg att ggc att gag gcc gac ccg gac agg ccc gac tgg cac gag tgg	771
Val Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp	
240 245 250	
ttc tcg cgc aga ctg cag ttc tgc cag tgg acg atc cag gcg aag ccg	819
Phe Ser Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro	
255 260 265 270	
gga cac ccg ctg ctg cgc gag ctg atc atc cgg atc gtg gag gag acg	867
Gly His Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr	
275 280 285	
ttc cgc aaa cag cac atg ggc gtt ttg aaa aga gtg gaa ggc aag gac	915
Phe Arg Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp	

290	295	300	
tcg ggc gca gat atc atg cag tgg aca gga ccg ggg ata ttt aca gac			963
Ser Gly Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp			
305	310	315	
act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc			1011
Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly			
320	325	330	
gac ggg tac ggc gtg ggg tcg ttg tat tgg cgc aag cac ggc aaa tat			1059
Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr			
335	340	345	350
aag ctg aaa aag aca gaa att aac aag aat aac gag cca ttg cat tct			1107
Lys Leu Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser			
355	360	365	
gag gac cag ctt atc aac tgg agg tcg ctg acc aac atg gac aag cca			1155
Glu Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro			
370	375	380	
aag atc atg ggg gac gta atg gtg tta cca atc acg agc ttt agt ccg			1203
Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro			
385	390	395	
aac gtg ggg cac atg ggc tca aag agc agc tca gat agg ctg gca ttt			1251
Asn Val Gly His Met Gly Ser Lys Ser Ser Ser Asp Arg Leu Ala Phe			
400	405	410	
gtg gag cat tta ttt tct ggc agc tgg aag cca aaa aac aaa			1293
Val Glu His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys			
415	420	425	
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 <212> PRT
 <213> Hansenula polymorpha

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35 40 45

Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu

50

55

60

Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His Leu Asn
 65 70 75 80

Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr Phe Tyr
 85 90 95

Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr
 100 105 110

Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr Arg Arg
 115 120 125

Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr His Leu
 130 135 140

Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr Ala Asn
 145 150 155 160

Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn Ile Met
 165 170 175

Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly Gly Thr
 180 185 190

Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp Trp Ala
 195 200 205

Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala Asp Leu
 210 215 220

Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu Val Ile
 225 230 235 240

Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp Phe Ser
 245 250 255

Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro Gly His
 260 265 270

Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr Phe Arg
 275 280 285

Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp Ser Gly
290 295 300

Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp Thr Leu
305 310 315 320

Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly Asp Gly
325 330 335

Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr Lys Leu
340 345 350

Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser Glu Asp
355 360 365

Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro Lys Ile
370 375 380

Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro Asn Val
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 35 40 45

 Lys Ile Val Ser Glu Tyr Leu Asn Asn Phe Tyr Lys Leu Asn Pro Lys
 50 55 60

 Phe Arg Gly Ala Asn Pro Tyr Asp Ala Ala Val Thr Ala Glu Arg Leu
 65 70 75 80

 Ala Lys Phe Phe Pro Tyr Asp Asn Ser Ala Arg Arg Ile Glu Lys Ser
 85 90 95

 Ile Trp Gln Met Trp Lys Val Pro Ser Thr Asp Pro Asp Phe Pro His
 100 105 110

 Lys Glu Leu Val Asn Lys Trp Lys Asn Glu Asn Pro Thr Tyr Lys Tyr
 115 120 125

 Asn Leu Leu Thr Asp Asp Glu Ile Leu Glu Ile Leu Arg Ile Arg Phe
 130 135 140

 Lys Asp Thr Val Pro Glu Val Leu Glu Ala Phe Glu Met Leu Pro Asn

145	150	155	160
Lys Ile Ile Arg Ser Asp Phe Ala Arg Tyr Leu Leu Ile Phe Leu Asn			
165	170	175	
Gly Gly Val Tyr Ala Asp Ile Asp Thr Asp Leu Gln Lys Pro Val Asp			
180	185	190	
Thr Trp Phe Asp Ser Asp Arg Asn Val Gly Phe Val Val Ala Val Glu			
195	200	205	
Glu Asp Ile Asn Val Glu Asn Trp Glu His Tyr Met Thr Arg Arg Ile			
210	215	220	
Gln Phe Glu Gln Trp Thr Phe Lys Ala Lys Ala Lys His Pro Ile Leu			
225	230	235	240
Arg Lys Leu Ile Ala Lys Ile Val Glu Thr Thr Phe Gln Ala Lys Lys			
245	250	255	
Asn Asp Lys Leu Gln Ala Tyr Tyr Lys Asp Phe Lys Gly Val Asp Arg			
260	265	270	
Cys Ala Ser Val Asp Ile Met Val Trp Thr Gly Pro Val Val Trp Thr			
275	280	285	
Asp Thr Ile Tyr Ala His Leu Asn Ser Ile Pro Ser Pro Thr Ile Val			
290	295	300	
Asp Ile Asp His Gln Arg Asp Ile Ala Gly Glu Leu Tyr Gly Pro Glu			
305	310	315	320
Thr Gly Glu Gly Asp Val Ile Ser Trp Arg Phe Phe Ala Gly Leu Arg			
325	330	335	
Ala Pro Val Met Ile Asp Asp Val Val Ile Tyr Pro Arg Ala Ser Phe			
340	345	350	
Arg Glu Asp Lys Glu Asn Asn Cys Gly Lys Tyr Cys Tyr Val His His			
355	360	365	
His Phe Gly Gly Ser Trp Lys Asn Asn Gly Lys Gly Glu Ile Lys Pro			
370	375	380	

Gly Met Glu Gly Tyr Glu Gly Glu Asp Pro Asn Glu Val Glu Glu Leu
385 390 395 400

Arg Lys Asn Asp Val Ser Lys Arg Asp Val Ile Pro Gly Glu Ser Lys
405 410 415

Asp Val Ala Pro Val Lys Lys Leu Ala Lys Arg Cys Ala Tyr Pro Tyr
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Thr Pro Tyr
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<213> Candida albicans

<220>
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<222> (384)..(385)
<223> Xaa can be any naturally occurring amino acid

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Ser Leu Ser Ser Pro Thr Ser Thr His Lys Thr Glu Tyr Asn Ser Pro
35 40 45

Lys Leu Gln Leu Ala Lys Glu Leu Glu Leu Asn Ser Asn Trp Lys Glu
50 55 60

Leu Gly Leu Asn Phe Gln Pro Asn Lys Lys Tyr Ser Leu Pro Asp Glu
65 70 75 80

Ser Thr Leu Arg Gln Gln Leu Ser Tyr Gln Phe Pro Tyr Asp Glu Ser
85 90 95

Lys Pro Phe Pro Lys Asn Ile Trp Gln Thr Trp Lys Val Gly Ile Asp
100 105 110

Glu Lys Ser Phe Pro Lys Arg Tyr Leu Lys Tyr Gln Gln Thr Trp Glu
115 120 12